Applicants acknowledge the objection to the drawings by the Draftsperson as set forth on Form PTO-948. Corrected drawings are attached herewith. Regarding the Information Disclosure Statement, the Examiner alleges that references BL, BM and DJ recite Accession Numbers which could not be located in the National Center for Biotechnology Information (NCBI) database or in the Derwent sequence database. Copies of DJ, BL and BM are enclosed herewith for the Examiner's convenience.

Rejection under 35 U.S.C. § 102

The Examiner rejects claims 21, 66, 69 and 71-72 under 35 U.S.C. § 102(b) as anticipated by Bandman *et al.* (U.S. 5,786,148). The Examiner alleges that Bandman *et al.* teach a HPSK protein sequence 88.8% identical to SEQ ID NO: 525 of the instant application. The Examiner further alleges that Bandman *et al.* teach that the protein sequence disclosed therein may be combined with adjuvants, physiological carriers or be used to produce antibodies.

Applicants respectfully traverse this rejection. The presently pending claims are drawn to isolated polypeptides having at least 90% identity to the entirety of SEQ ID NO: 525 and isolated polypeptide having at least 90% identity to a polypeptide comprising amino acids 1-39 of SEQ ID NO: 525; wherein the polypeptide contains an amino acid sequence capable of stimulating human T-cells.

"A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). "The identical invention must be shown in as complete detail as it is contained in the...claim." *Richardson v. Suzuki Motor Co.*, 868 F.2d 1226, 1236, 9 USPQ2d 1913, 1920 (Fed. Cir. 1989). Moreover, the elements must be arranged as required by the claim. *In re Bond*, 910 F.2d 831, 15 USPQ2d 1566 (Fed. Cir. 1990). See also MPEP 2131.

Applicants submit that Bandman *et al.* does not anticipate the polypeptides currently claimed by the applicants. More particularly, Bandman *et al.*, while disclosing a sequence having some degree of similarity to SEQ ID NO: 525, does not disclose a sequence having at least 90% identity to the entirety of SEQ ID NO: 525, as currently claimed, much less that the polypeptide contains an amino acid sequence capable of stimulating human T-cells.

Applicants further submit that amino acids 1-39 of SEQ ID NO: 525 are unique to SEQ ID NO: 525, and thus are not contained in the polypeptide disclosed by Bandman *et al.* Consequently, Bandman *et al.* fails to anticipate the subject matter of new claims 73 and 75, drawn to isolated polypeptides comprising amino acid residues 1-39 of SEQ ID NO: 525. Accordingly, in view of the above amendment and remarks, applicants respectfully request reconsideration and withdrawal of the Examiner's rejection under 35 U.S.C. § 102(b).

The Examiner also rejects claims 21, 66-69 and 71-72 under 35 U.S.C. § 102(e) as anticipated by Gimeno *et al.* (U.S. 5,955,306). In particular the Examiner alleges that Gimeno *et al.* teach a protein that is 97.6% identical to SEQ ID NO:525 of the instant application. The Examiner further alleges that Gimeno *et al.* teach that immunogenic proteins may be mixed with adjuvants and/or formulated in physiological acceptable carriers.

Applicants respectfully traverse this rejection. As noted above, the currently claimed invention is drawn to isolated polypeptides having at least 90% identity to the entirety of SEQ ID NO: 525; and isolated polypeptides having at least 90% identity to a polypeptide comprising amino acids 1-39 of SEQ ID NO: 525. Applicants submit that Gimeno *et al.*, while describing a sequence having some degree of similarity with the polypeptide of SEQ ID NO: 525, does not specifically describe in complete detail the polypeptides as currently claimed by the applicants, much less that the polypeptides contain an amino acid sequence capable of stimulating human T-cells. Accordingly, the instant claims, as amended hereinabove, are indeed novel over Gimeno *et al.* Reconsideration and withdrawal of the Examiner's rejection are thus respectfully requested.

Rejection under 35 U.S.C. § 103

The Examiner rejects claims 21-22, 66, 69 and 71-72 under 35 U.S.C. § 103(a) as unpatentable over Bandman *et al.* in view of Hauser *et al.* (U.S. 5,776,468), and over Gimeno *et al.* in view of Hauser *et al.* (U.S. 5,776,468). In particular the Examiner alleges that Bandman *et al.* and Gimeno *et al.* teach the polypeptide according to the instant application and that Hauser *et al.* provides an immunostimulant which induces a type I response.

As noted above, neither Bandman *et al.* nor Gimeno *et al.* teach the currently claimed polypeptides related to SEQ ID NO: 525. Moreover, the deficiencies of Bandman *et al.*

and Gimeno *et al.* are not remedied by Houser *et al.*, which merely discloses an immunostimulant, but does not disclose a polypeptide presently claimed by Applicants. Accordingly, Applicants submit that neither Bandman *et al.*, nor Gimeno *et al.*, alone or in combination with Hauser *et al.*, would lead the skilled artisan to any expectation of arriving at the Applicants' claimed invention when the combined disclosures of these references simply do not teach each and every element currently claimed. Applicants respectfully request that this rejection under 35 U.S.C. § 103(a) be withdrawn.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current Amendment, the first page of which is captioned "Version with Markings to Show Changes Made."

Favorable consideration and a Notice of Allowance are earnestly solicited. The Examiner is invited to contact the undersigned at (206) 694-4885 with any questions, comments and/or suggestions relating to this communication. Please credit any overpayment or charge any deficiency to Deposit Account No. 19-1090.

Respectfully submitted,

SEED Intellectual Property Law Group PLLC

Jeffrey Hundley, Ph.D., Patent Agent
Registration No. 42,676

JEH:sds
Enclosure:
Postcard
14 Sheets Drawings (Figs. 1-12B)
3 References

701 Fifth Avenue, Suite 6300
Seattle, Washington 98104-7092
Phone: (206) 622-4900
Fax: (206) 682-6031

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Please replace the paragraph on page 1, under the heading "CROSS REFERENCE TO RELATED APPLICATIONS" with the following rewritten paragraph.

--This application is a continuation-in-part of U.S. Patent Application No. 09/443,686, filed November 18, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/352,616, filed July 13, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/288,946, filed April 9, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/232,149, filed January 15, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/159,812, filed September 23, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/115,453, filed July 14, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/030,607, filed February 25, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/020,956, filed February 9, 1998, which is a continuation-in-part of U.S. Patent Application No. 08/904,804, filed August 1, 1997, which is a continuation-in-part of U.S. Patent Application No. 08/806,099, filed February 25, 1997.--

In the Claims:

Claims 66-71 have been canceled, claim 72 has been amended and claims 73-79 are newly added.

72. (Amended) A composition comprising an immunostimulant and an isolated polypeptide having at least 90% identity to the entirety of SEQ ID NO: 525, wherein the polypeptide contains an amino acid sequence capable of stimulating human T-cells. ~~according to any one of claims 65-70.~~

73. (New) A composition comprising an immunostimulant and an isolated polypeptide having at least 90% identity to a polypeptide comprising amino acids 1-39 of SEQ

ID NO: 525, wherein the polypeptide contains an amino acid sequence capable of stimulating human T-cells.

74. (New) A composition comprising an immunostimulant and an isolated polypeptide comprising SEQ ID NO: 525, wherein the polypeptide contains an amino acid sequence capable of stimulating human T-cells.

75. (New) A composition comprising an immunostimulant and an isolated polypeptide comprising amino acids 1-39 of SEQ ID NO: 525, wherein the polypeptide contains an amino acid sequence capable of stimulating human T-cells.

76. (New) The composition according to claim 72, wherein the polypeptide has at least 95% identity to the entirety of SEQ ID NO: 525.

77. (New) The composition according to any one of claims 72-76, wherein the immunostimulant is selected from the group consisting of a monophosphoryl lipid A, a CpG-containing oligonucleotide, a saponin, or a combination thereof.

78. (New) The composition according to any one of claims 72-76, wherein the immunostimulant is selected from the group consisting of 3D-MPL, QS21, or a combination thereof.

79. (New) The composition according to any one of claims 72-76, wherein the immunostimulant comprises 3D-MPL, QS21 and tocopherol in an oil-in-water emulsion.

D:\N\Portbl\iManage\BOBF\248157_1.DOC

Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

Inventor(s): Jiangchun Xu et al. Serial No. 09/483,672 Docket No. 210121.427C11

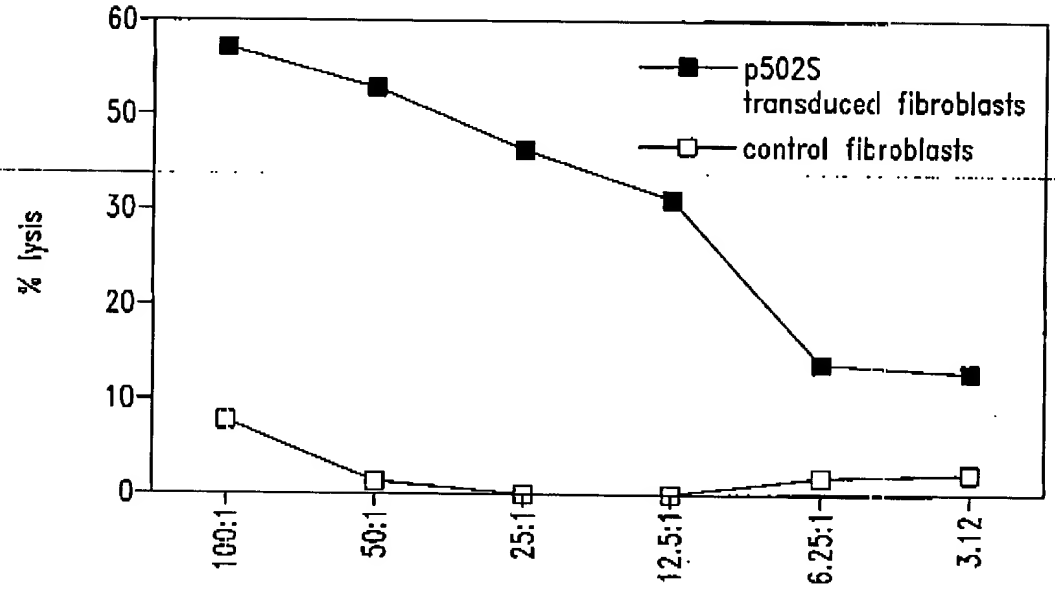


Fig. 1

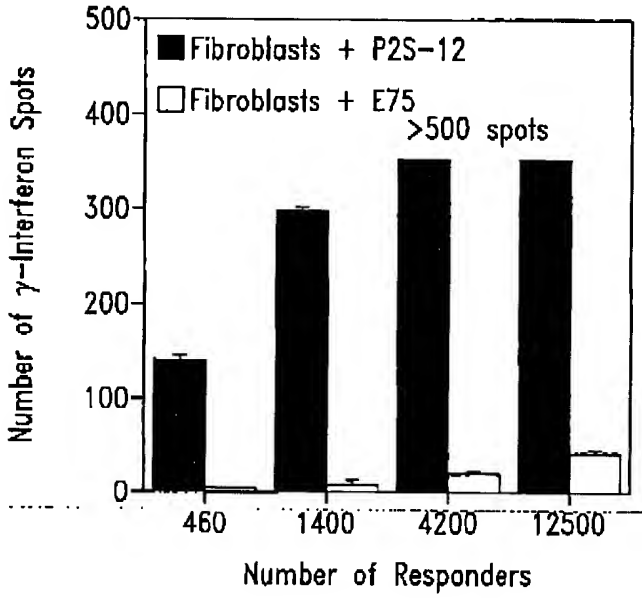

Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
500
400
300
200
100
0
460
1400
4200
12500
Number of Responders

Fig. 2A

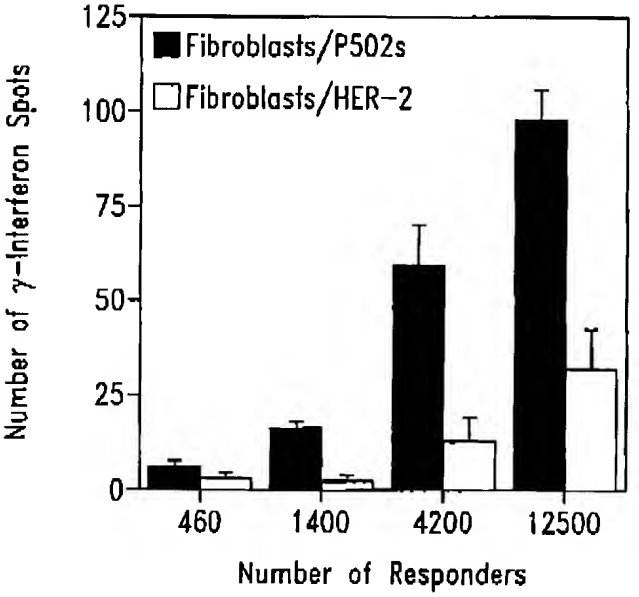

Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4200
12500
Number of Responders

Fig. 2B

Title: COMP[illegible]TIONS AND METHODS FOR THERAPY AND DIAGNOSI[illegible]F PROSTATE CANCER

Inventor(s): Jiangchun Xu et al. Serial No. 09/483,672 Docket No. 210121.427C11

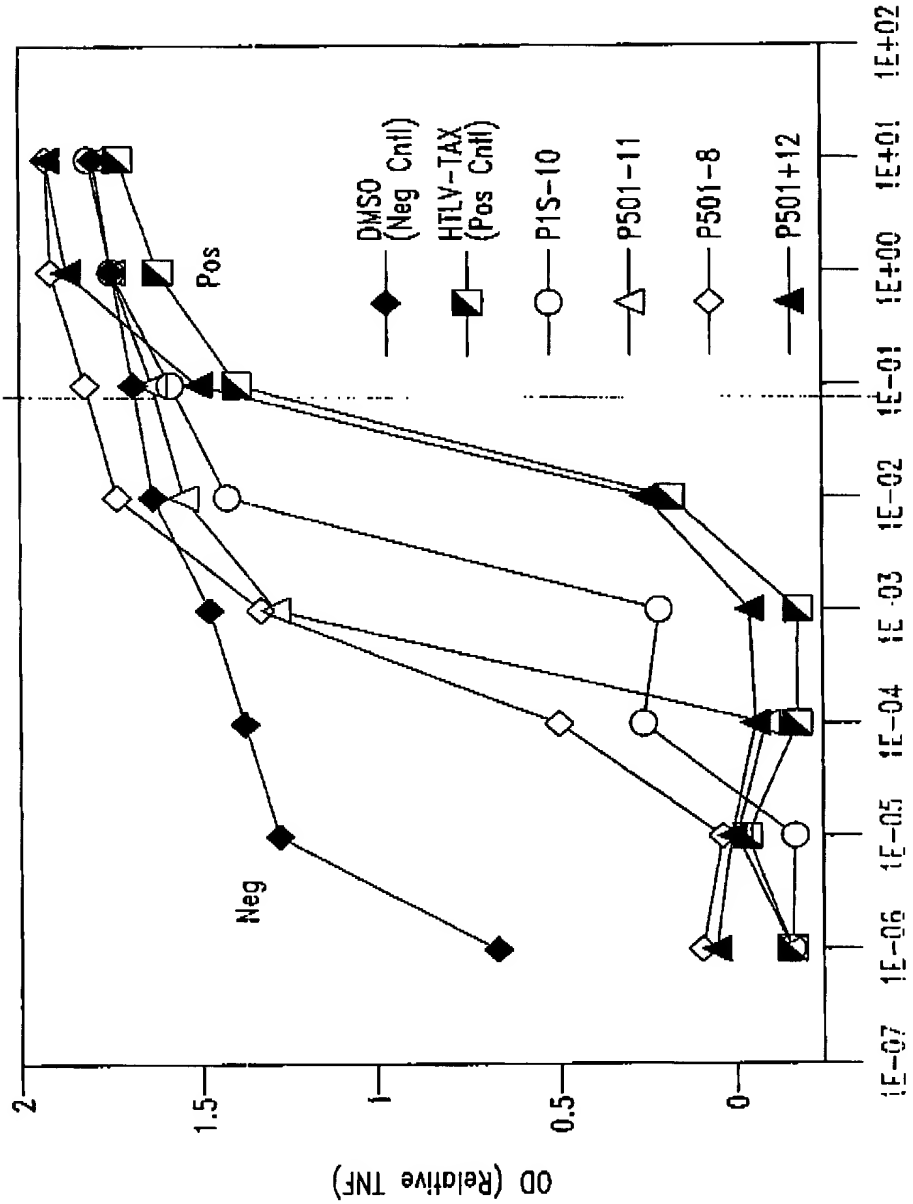


Fig. 3

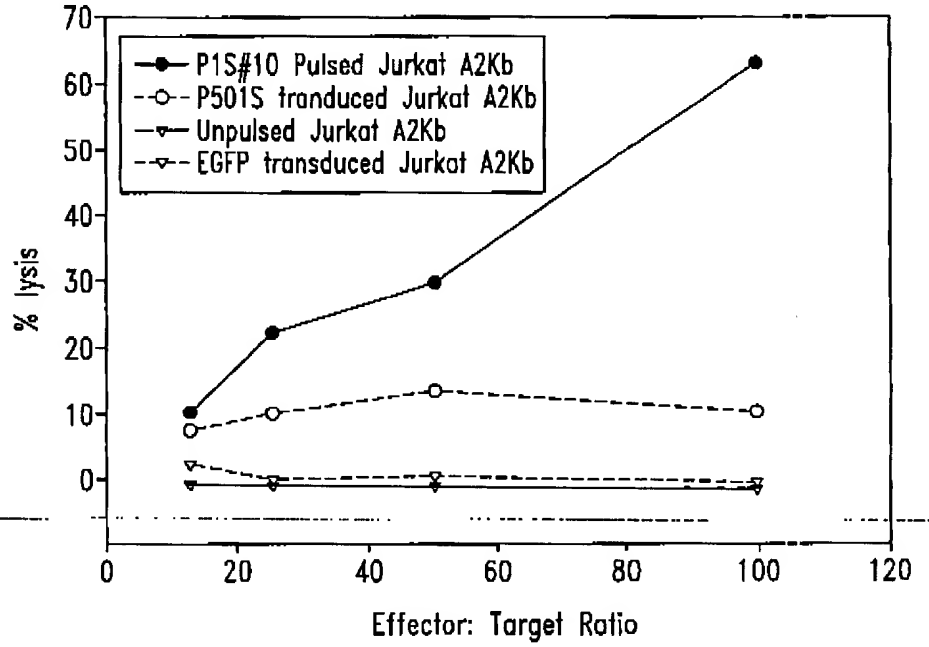

P1S#10 Pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Fig. 4

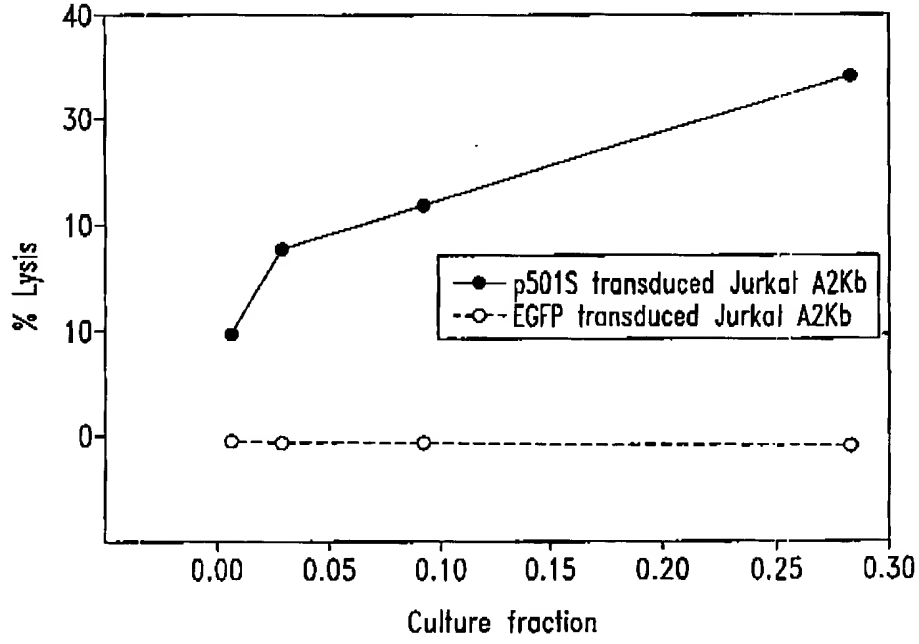

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
Culture fraction
0
10
10
30
40
0.00
0.05
0.10
0.15
0.20
0.25
0.30

Fig. 5

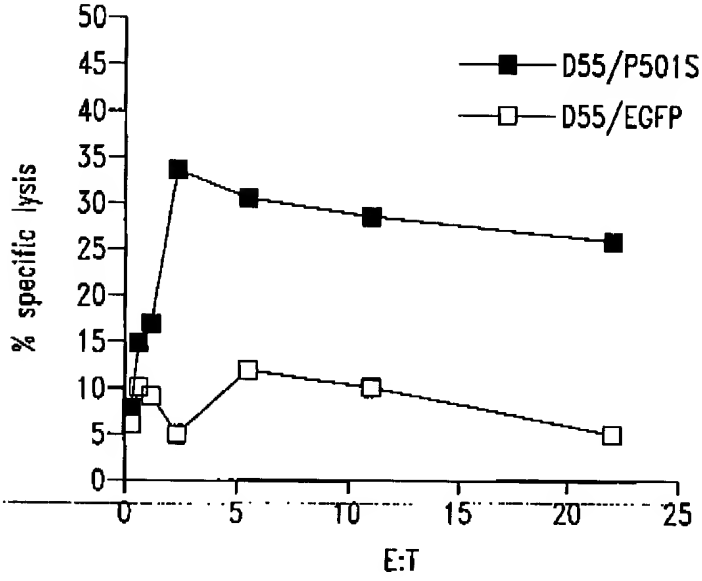

50
45
40
35
30
25
20
15
10
5
0
% specific lysis
0
5
10
15
20
25
E:T
D55/P501S
D55/EGFP

Fig. 6A

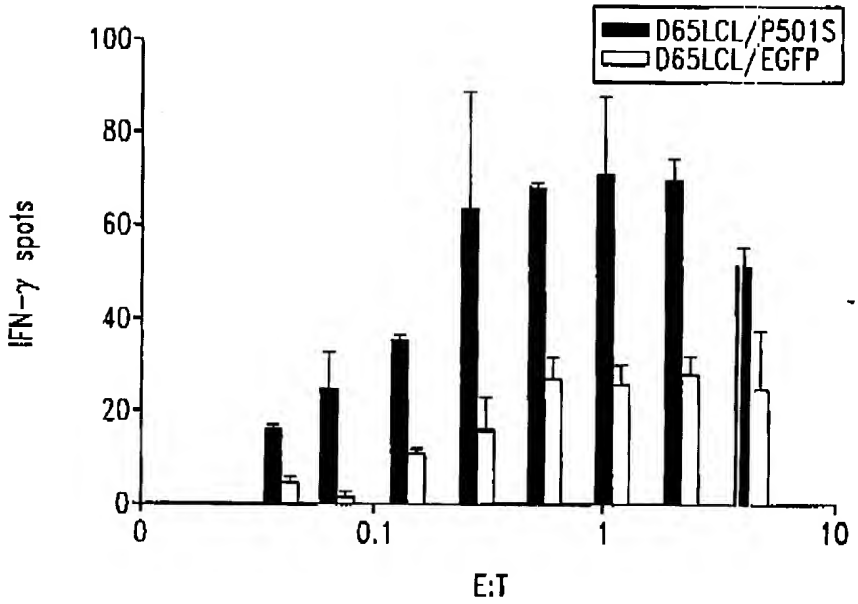
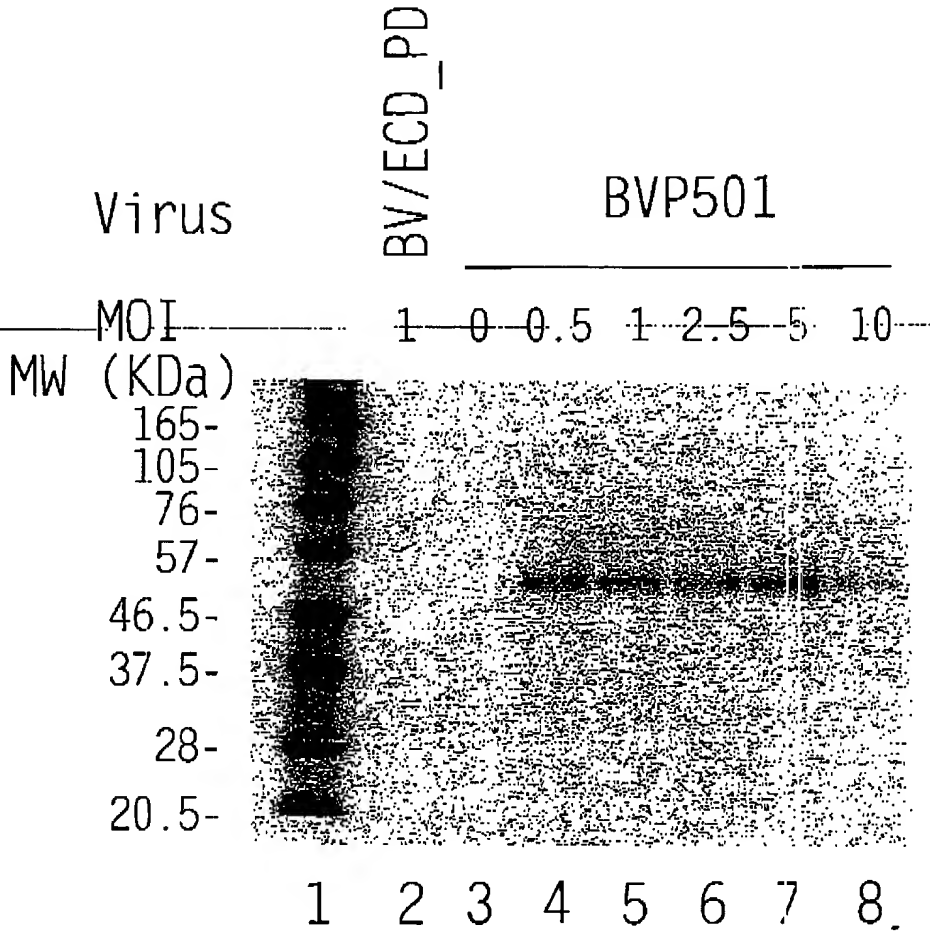

100
80
60
40
20
0
IFN-γ spots
0
0.1
1
10
E:T
D65LCL/P501S
D65LCL/EGFP

Fig. 6B

Title: COMP[illegible]TIONS AND METHODS FOR THERAPY AND DIAGNOS[illegible]F PROSTATE CANCER

Inventor(s): Jiangchun Xu et al. Serial No. 09/483,672 Docket No. 210121.427C11

Expression of P501S
by the Baculovirus Expression System



C 6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein mo[illegible]ecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

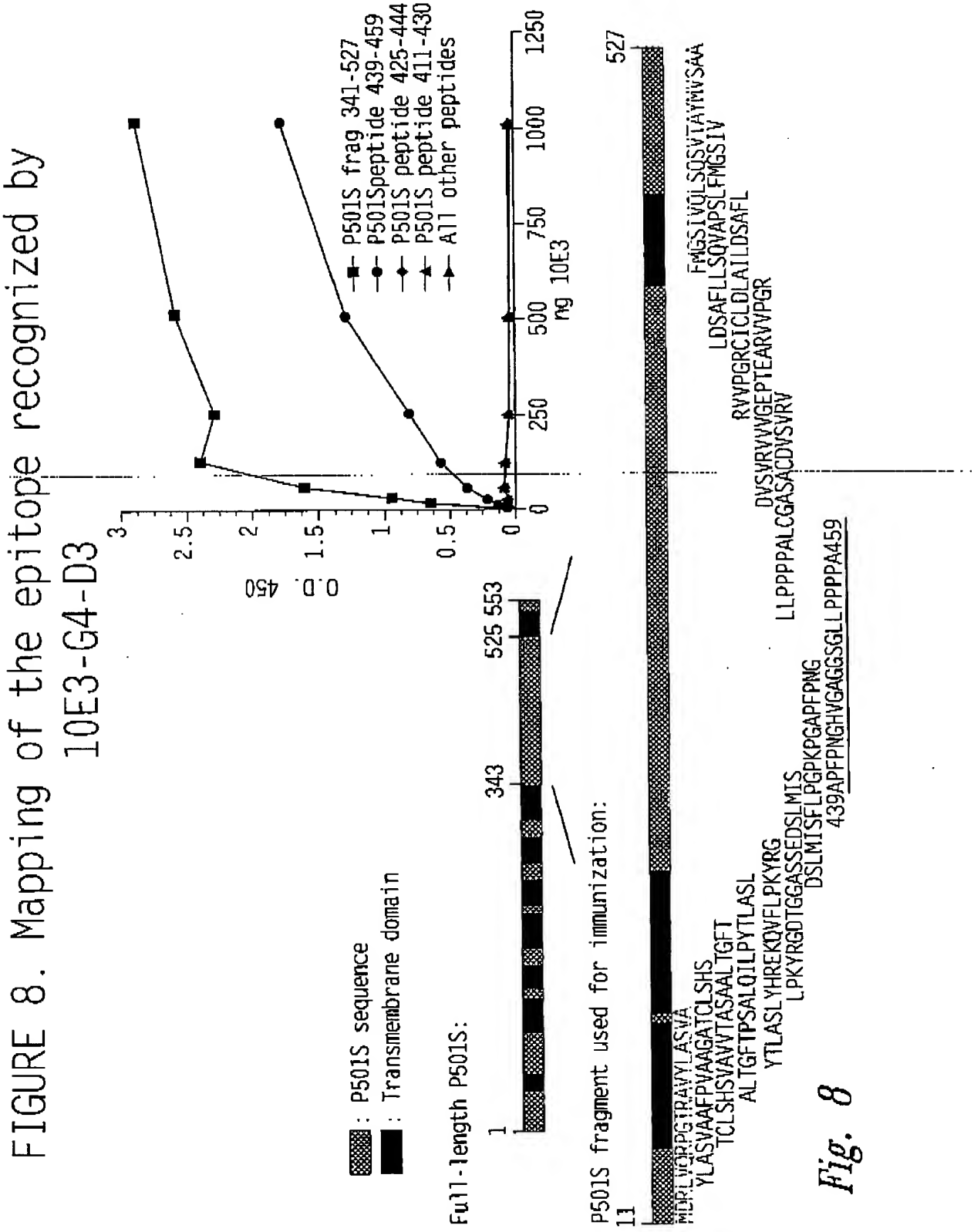


Fig. 8

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGVPRAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGACFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predictec intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283. 489-506.

Fig. 9

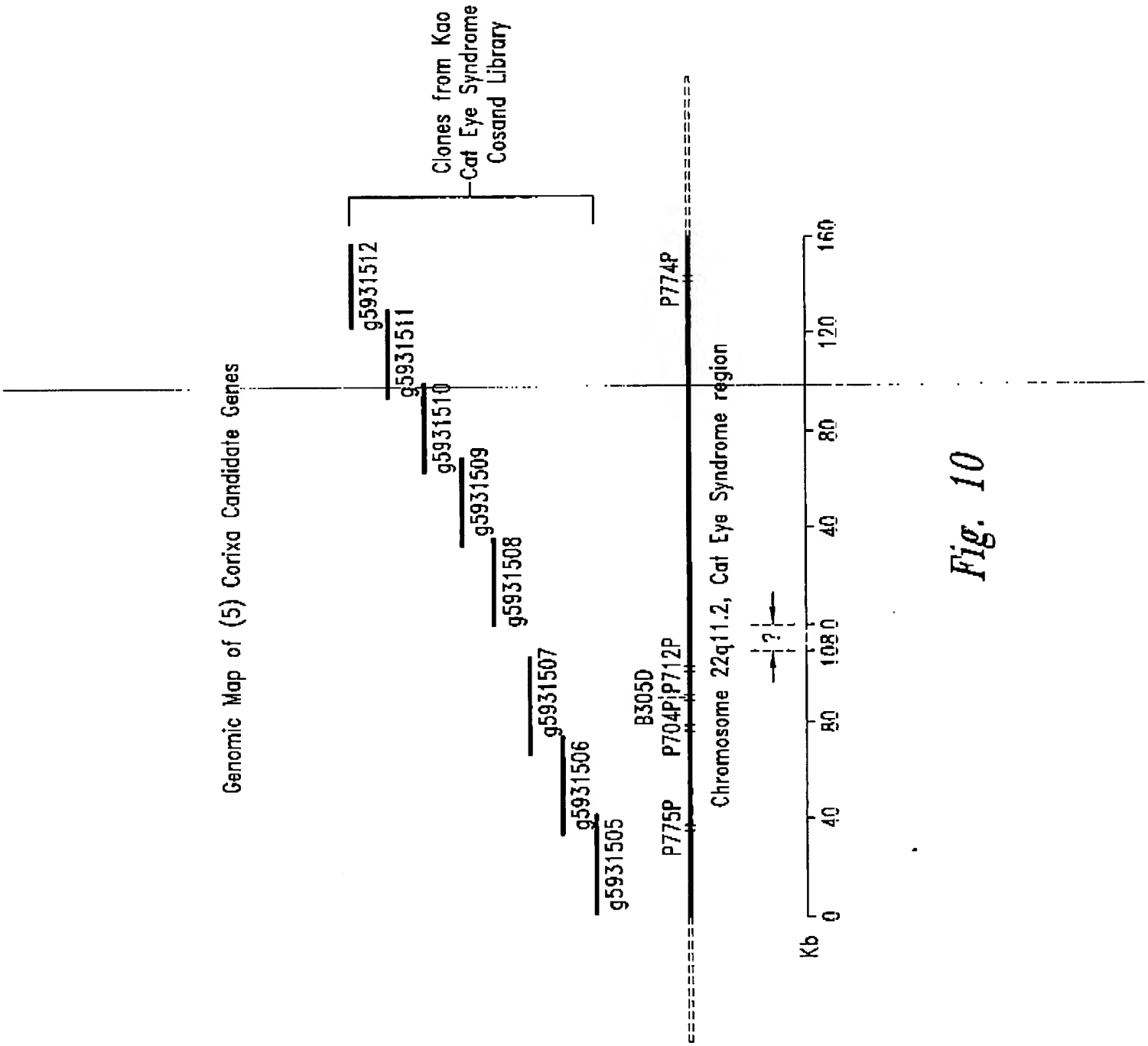

Genomic Map of (5) Corixa Candidate Genes
Clones from Kao Cat Eye Syndrome Cosand Library
g5931512
g5931511
g5931510
g5931509
g5931508
g5931507
g5931506
g5931505
P774P
B305D
P704P
P712P
P775P
Chromosome 22q11.2, Cat Eye Syndrome region
?
0
40
80
108
0
40
80
120
160
Kb

Fig. 10

Title: COMP[illegible]TIONS AND METHODS FOR THERAPY AND DIAGNOSI[illegible]E PROSTATE CANCER

Inventor(s): Jiangchun Xu et al. Serial No. 09/483,672 Docket No. 210121.427C11

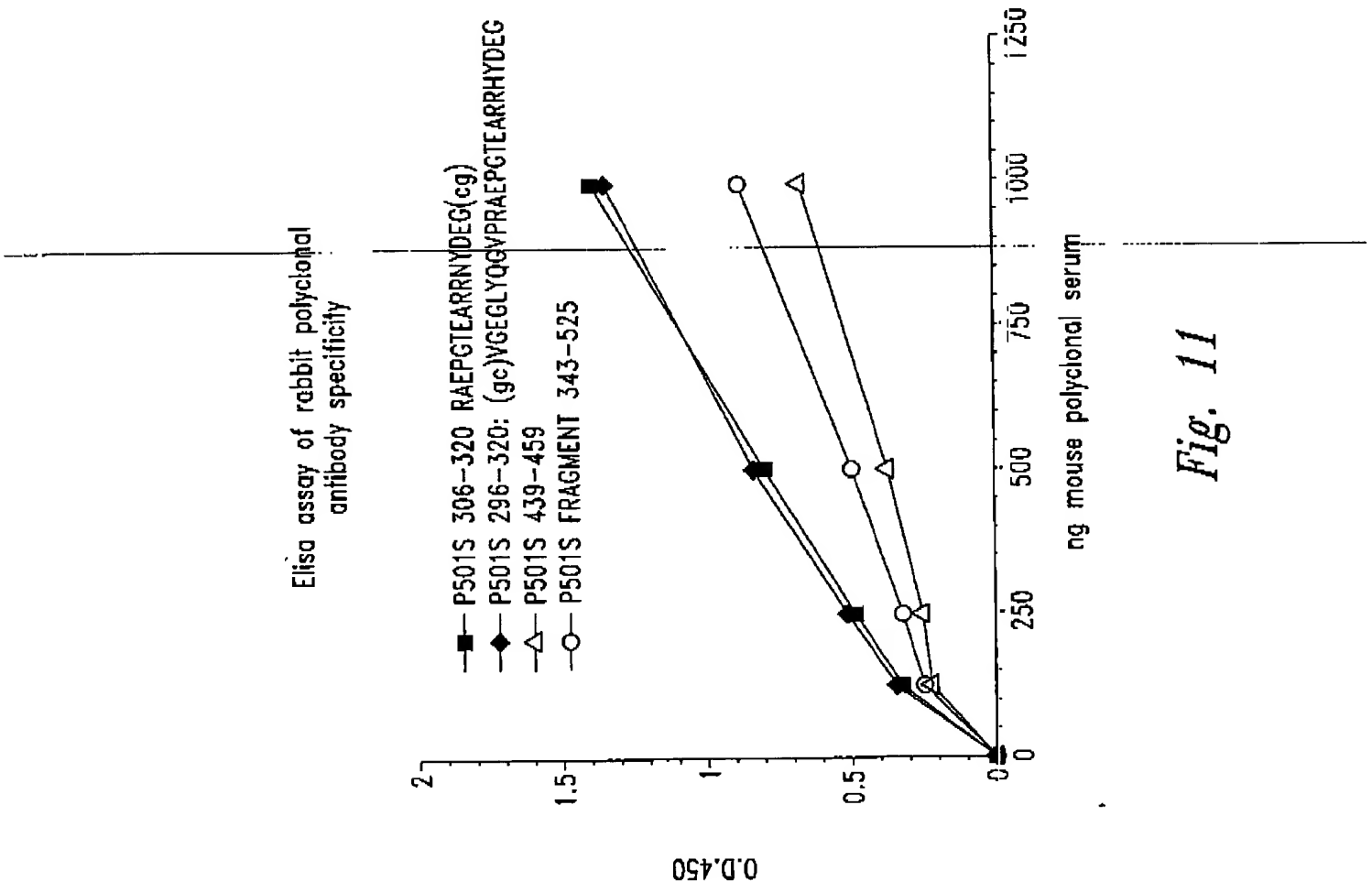


Fig. 11

GTCACTTAGG AAAAGGTGTC CTTTCGGGCA GCCGGGCTCA GCATGAGGAA CAGAAGGAAT 60
GACACTCTGG ACAGCACCCG GACCCTGTAC TCCAGCGCGT CTCGGAGCAC AGACTTGTCT 120
TACAGTGAAA GCGACTTGGT GAATTTTATT CAAGCAAATT TTAAGAAACG AGAATGTGTC 180
TTCTTTACCA AAGATTCCAA GGCCACGGAG AATGTGTGCA AGTGTGGCTA TGCCCAGAGC 240
CAGCACATGG AAGGCACCCA GATCAACCAA AGTGAGAAAT GGAACTACAA GAAACACACC 300
AAGGAATTTC CTACCGACGC CTTTGGGGAT ATTCAGTTTG AGACACTGGG GAAGAAAGGG 360
AAGTATATAC GTCTGTCCTG CGACACGGAC GCGGAAATCC TTTACGAGCT GCTGACCCAG 420
CACTGGCACC TGAAAACACC CAACCTGGTC ATTTCTGTGA CCGGGGGCGC CAAGAACTTC 480
GCCCTGAAGC CGCGCATGCG CAAGATCTTC AGCCGGCTCA TCTACATCGC GCAGTCCAAA 540
GGTGCTTGGA TTCTCACGGG AGGCACCCAT TATGGCCTGA CGAAGTACAT CGGGGAGGTG 600
GTGAGAGATA ACACCATCAG CAGGAGTTCA GAGGAGAATA TTGTGGCCAT TGGCATAGCA 660
GCTTGGGGCA TGGTCTCCAA CCGGGACACC CTCATCAGGA ATTGCGATGC TGAGGGCTAT 720
TTTTTAGCCC AGTACCTTAT GGATGACTTC ACAAGGGATC CACTGTATAT CCTGGACAAC 780
AACCACACAC ATTTGCTGCT CGTGGACAAT GGCTGTCATG GACATCCCAC TGTCGAAGCA 840
AAGCTCCGGA ATCAGCTAGA GAAGCATATC TCTGAGCGCA CTATTCAAGA TTCCAACTAT 900
GGTGGCAAGA TCCCCATTGT GTGTTTTGCC CAAGGAGGTG GAAAAGAGAC TTTGAAAGCC 960
ATCAATACCT CCATCAAAAA TAAAATTCCT TGTGTGGTGG TGGAAGGCTC GGGCCGGATC 1020
GCTGATGTGA TCGCTAGCCT GGTGGAGGTG GAGGATGCCC CGACATCTTC TGCCGTCAAG 1080
GAGAAGCTGG TGCGCTTTTT ACCCCGCACG GTGTCCCGGC TGTCTGAGGA GGAGACTGAG 1140
AGTTGGATCA AATGGCTCAA AGAAATTCTC GAATGTTCTC ACCTATTAAC AGTTATTAAA 1200
ATGGAAGAAG CTGGGGATGA AATTGTGAGC AATGCCATCT CCTACGCTCT ATACAAAGCC 1260
TTCAGCACCA GTGAGCAAGA CAAGGATAAC TGGAATGGGC AGCTGAAGCT TCTGCTGGAG 1320
TGGAACCAGC TGGACTTAGC CAATGATGAG ATTTTCACCA ATGACCGCCG ATGGGAGTCT 1380
GCTGACCTTC AAGAAGTCAT GTTTACGGCT CTCATAAAGG ACAGACCCAA GTTTGTCCGC 1440
CTCTTTCTGG AGAATGGCTT GAACCTACGG AAGTTTCTCA CCCATGATGT CCTCACTGAA 1500
CTCTTCTCCA ACCACTTCAG CACGCTTGTG TACCGGAATC TGCAGATCGC CAAGAATTCC 1560
TATAATGATG CCCTCCTCAC GTTTGTCTGG AAACTGGTTG CGAACTTCCG AAGAGGCTTC 1620
CGGAAGGAAG ACAGAAATGG CCGGGACGAG ATGGACATAG AACTCCACGA CGTGTCTCCT 1680
ATTACTCGGC ACCCCCTGCA AGCTCTCTTC ATCTGGGCCA TTCTTCAGAA TAAGAAGGAA 1740
CTCTCCAAAG TCATTTGGGA GCAGACCAGG GGCTGCACTC TGGCAGCCCT GGGAGCCAGC 1800
AAGCTTCTGA AGACTCTGGC CAAAGTGAAG AACGACATCA ATGCTGCTGG GGAGTCCGAG 1860
GAGCTGGCTA ATGAGTACGA GACCCGGGCT GTTGAGCTGT TCACTGAGTG TTACAGCAGC 1920
GATGAAGACT TGGCAGAACA GCTGCTGGTC TATTCCTGTG AAGCTTGGGG TGGAAGCAAC 1980
TGTCTGGAGC TGGCGGTGGA GGCCACAGAC CAGCATTTCA CCGCCCAGCC TGGGGTCCAG 2040
AATTTTCTTT CTAAGCAATG GTATGGAGAG ATTTCCCGAG ACACCAAGAA CTGGAAGATT 2100

Fig. 12A (1)

ATCCTGTGTC TGTTTATTAT ACCCTTGGTG GGCTGTGGCT TTGTATCATT TAGGAAGAAA 2160
CCTGTCGACA AGCACAAGAA GCTGCTTTGG TACTATGTGG CGTTCTTCAC CTCCCCCTTC 2220
GTGGTCTTCT CCTGGAATGT GGTCTTCTAC ATCGCCTTCC TCCTGCTGTT TCCCTACGTG 2280
CTGCTCATGG ATTTCCATTC GGTGCCACAC CCCCCCGAGC TGGTCCTGTA CTCGCTGGTC 2340
TTTGTCCTCT TCTGTGATGA AGTGAGACAG TGGTACGTAA ATGGGGTGAA TTATTTTACT 2400
GACCTGTGGA ATGTGATGGA CACGCTGGGG CTTTTTTACT TCATAGCAGG AATTGTATTT 2460
CGGCTCCACT CTTCTAATAA AAGCTCTTTG TATTCTGGAC GAGTCATTTT CTGTCTGGAC 2520
TACATTATTT TCACTCTAAG ATTGATCCAC ATTTTTACTG TAAGCAGAAA CTTAGGACCC 2580
AAGATTATAA TGCTGCAGAG GATGCTGATC GATGTGTTCT TCTTCCTGTT CCTCTTTGCG 2640
GTGTGGATGG TGGCCTTTGG CGTGGCCAGG CAAGGGATCC TTAGGCAGAA TGAGCAGCGC 2700
TGGAGGTGGA TATTCCGTTC GGTCATCTAC GAGCCCTACC TGGCCATGTT CGGCCAGGTG 2760
CCCAGTGACG TGGATGGTAC CACGTATGAC TTTGCCCACT GCACCTTCAC TGGGAATGAG 2820
TCCAAGCCAC TGTGTGTGGA GCTGGATGAG CACAACCTGC CCCGGTTCCC CGAGTGGATC 2880
ACCATCCCCC TGGTGTGCAT CTACATGTTA TCCACCAACA TCCTGCTGGT CAACCTGCTG 2940
GTCGCCATGT TTGGCTACAC GGTGGGCACC GTCCAGGAGA ACAATGACCA GGTCTGGAAG 3000
~~TTCCAGAGGT ACTTCCTGGT GCAGGAGTAC TGCAGCCGCC TCAATATCCC CTTCCCCTTC 3060~~
ATCGTCTTCG CTTACTTCTA CATGGTGGTG AAGAAGTGCT TCAAGTGTTG CTGCAAGGAG 3120
AAAAACATGG AGTCTTCTGT CTGCTGTTTC AAAAATGAAG ACAATGAGAC TCTGGCATGG 3180
GAGGGTGTCA TGAAGGAAAA CTACCTTGTC AAGATCAACA CAAAAGCCAA CGACACCTCA 3240
GAGGAAATGA GGCATCGATT TAGACAACTG GATACAAAGC TTAATGATCT CAAGGGTCTT 3300
CTGAAAGAGA TTGCTAATAA AATCAAATAA AACTGTATGA AACTCTAATG GAGAAAAATC 3360
TAATTATAGC AAGATCATAT TAAGGAATGC TGATGAACAA TTTTGCTATC GACTACTAAA 3420
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AGACCTTGAG AATAAAGTGT GTGATTGGTT TCATACTTGA AGACGGATAT AAAGGAAGAA 3540
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GACTGGAGGT TGATAGTTTA AGTGTGTTCT TACCGCCTCC TTTTTCCTTT AATCTTATTT 3660
TTGATGAACA CATATATAGG AGAACATCTA TCCTATGAAT AAGAACCTGG TCATGCTTTA 3720
CTCCTGTATT GTTATTTTGT TCATTTCCAA TTGATTCTCT ACTTTTCCCT TTTTTGTATT 3780
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TCTTACCTGT CAGAGGAGGT GACAAGGCAG TCTCTTGCTC TCTTGGACTC ACCAGGCTCC 3960
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GAATCCTATT GCTGTATTTG GGAAAATTTT CCAAGGTTAG ATTCCAATAA ATATCTATTT 4500
ATTATTAAAT ATTAAAATAT CGATTTATTA TTAAAACCAT TTATAAGGCT

Fig. 12A (2)

TTTTCATAAA	4560
TGTATAGCAA ATAGGAATTA TTAACTTGAG CATAAGATAT GAGATACATG AACCTGAACT	4620
ATTAAAATAA AATATTATAT TTAACCCTAG TTTAAGAAGA AGTCAATATG CTTATTTAAA	4680
TATTATGGAT GGTGGGCAGA TCACTTGAGG TCAGGAGTTC GAGACCAGCC TGGCCAACAT	4740
GGCAAAACCA CATCTCTACT AAAAATAAAA AAATTAGCTG GGTGTGGTGG TGCACTCCTG	4800
TAATCCCAGC TACTCAGAAG GCTGAGGTAC AAGAATTGCT GGAACCTGGG AGGCGGAGGT	4860
TGCAGTGAAC CAAGATTGCA CCACTGCACT CCAGCCGGGG TGACAGAGTG AGACTCCGAC	4920
TGAAAATAAA TAAATAAATA AATAAATAAA TAAATAAATA AATATTATGG ATGGTGAAGG	4980
GAATGGTATA GAATTGGAGA GATTATCTTA CTGAACACCT GTAGTCCCAG CTTTCTCTGG	5040
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CTGGGCAGTA GTGAAAATAA CTACTCACAA CATTCACTAT GTTTGCAAGG AATTAACACA	5280
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AACTTGCATT AGAGAGGGAA CTGTTAAATG TTTTCAACCC AGTTCATCTG GTGGATGTTT	5400
~~TTGCAGGTTA CTCTGAGAAT TTTGCTTATG AAAAATCATT ATTTTTAGTG TAGTTCACAA~~	~~5460~~
TAATGTATTG AACATACTTC TAATCAAAGG TGCTATGTCC TTGTGTATGG TACTAAATGT	5520
GTCCTGTGTA CTTTTGCACA ACTGAGAATC CTGCGGCTTG GTTTAATGAG TGTGTTCATG	5580
AAATAAATAA TGGAGGAATT GTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	5640
AAAAAAAAAA AAAAAAAAAA AAAAAAAA	5668

Fig. 12A (3)

MRNRRNDTLDSTRTLYSSASRSTDLSYSESDLVNFIQANFKKRECVFFTKDSKATEWVCKCGYAQSQHME
GTQINQSEKWNYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT
GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV
RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN
HFSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI
LQNKKELSKVIWEQTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDL
AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPLVGCGF
VSFRKKPVDKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHFPELVLYSLVFVLF
CDEVRQWYVNGVNYFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTV
SRNLGPKIIMLQRMLIDVFFFLFLFAVWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDV
DGTTYDFAHCTFTGNESKPLCVELDEHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMFGYTVGTVQEN
NDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM
KENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKIK

Fig. 12B

L3 ANSWER 1 OF 1 DGENE COPYRIGHT 2001 DERWENT INFORMATION LTD
AN AAV58522 cDNA DGENE
TI Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
IN Dillon D C; Xu J
PA (CORI-N) CORIXA CORP.
PI WO 9837418 A2 19980827 141p
AI WO 1998-US3690 19980225
PRAI US 1998-904809 19980209
US 1997-806596 19970225
US 1997-904809 19970801
PSL Claim 1; Page 56
DED 08 DEC 1998 (first entry)
DT Patent
LA English
OS 1998-480805 [41]
DESC Prostate tumour specific gene clone P20.
KW Prostate tumour specific gene; human; prostate cancer; detection; therapy; ss.
ORGN Homo sapiens.
AB This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.
NA 43 A; 68 C; 68 G; 55 T; 0 other
SQL 234
SEQ

```
  1 acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa
 51 tccgtgtccg agtctgacac catccggagc atcagcattg cttcgcagtg
101 ccctaccgcg gggaactctt gcctcgtttc tggctggggt ctgctggcga
151 acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgcct
```

L4 ANSWER 1 OF 1 DGENE COPYRIGHT 2001 DERWENT INFORMATION LTD
AN AAV61287 cDNA DGENE
TI Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer
IN Dillon D C; Xu J
PA (CORI-N) CORIXA CORP.
PI WO 9837093 A2 19980827 130p
AI WO 1998-US3492 19980225
PRAI US 1998-20956 19980209
US 1997-806099 19970225
US 1997-904804 19970801
PSL Claim 12; Page 61
DED 06 JAN 1999 (first entry)
DT Patent
LA English
OS 1998-609886 [51]
DESC cDNA sequence of prostate tumour clone P80.
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
ORGN Homo sapiens.
AB The present sequence is a DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

NA 86 A; 105 C; 94 G; 100 T; 0 other
SQL 385
SEQ

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101 gacatcaggt ctgagagttc ccctttaaa aaaggggact tgcttaaaaa
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201 cttttgagag agttctcctc tgagacctga tctttagagg ctgggcagtc
251 ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg
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NCBI Protein

Search Protein for

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1: GI = "4758960" [GenPept] kallikrein 4 (prostase, ena... PubMed Related Seque

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LOCUS       NP_004908     254 aa                    PRI       18-MAR-2000
DEFINITION  kallikrein 4 (prostase, enamel matrix, prostate) [Homo sapiens].
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PID         g4758960
VERSION     NP_004908.1  GI:4758960
DBSOURCE    REFSEQ: accession NM_004917.1
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 254)
  AUTHORS   Nelson PS, Gan L, Ferguson C, Moss P, Gelinas R, Hood L and Wang K.
  TITLE     Molecular cloning and characterization of prostase, an
            androgen-regulated serine protease with prostate-restricted
            expression
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (6), 3114-3119 (1999)
  MEDLINE   99179024
   PUBMED   10077646
REFERENCE   2  (residues 1 to 254)
  AUTHORS   Stephenson SA, Verity K, Ashworth LK and Clements JA.
  TITLE     Localization of a new prostate-specific antigen-related serine
            protease gene, KLK4, is evidence for an expanded human kallikrein
            gene family cluster on chromosome 19q13.3-13.4
  JOURNAL   J. Biol. Chem. 274 (33), 23210-23214 (1999)
  MEDLINE   99367447
   PUBMED   10438493
REFERENCE   3  (residues 1 to 254)
  AUTHORS   Yousef GM, Obiezu CV, Luo LY, Black MH and Diamandis EP.
  TITLE     Prostase/KLK-L1 is a new member of the human kallikrein gene
            family, is expressed in prostate and breast tissues, and is
            hormonally regulated
  JOURNAL   Cancer Res. 59 (17), 4252-4256 (1999)
  MEDLINE   99413477
   PUBMED   10485467
REFERENCE   4  (residues 1 to 254)
  AUTHORS   DuPont BR, Hu CC, Reveles X and Simmer JP.
  TITLE     Assignment of serine protease 17 (PRSS17) to human chromosome bands
            19q13.3-->q13.4 by in situ hybridization
  JOURNAL   Cytogenet. Cell Genet. 86 (3-4), 212-213 (1999)
  MEDLINE   20044607
   PUBMED   10575207
COMMENT     REFSEQ: The reference sequence was derived from AF113147.1.
            PROVISIONAL RefSeq: This is a provisional reference sequence record
            that has not yet been subject to human review. The final curated
            reference sequence record may be somewhat different from this one.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..254
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                     /chromosome="19"
                     /map="19q13.3-q13.4"
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                     prostate)"
     CDS             1..254
                     /gene="KLK4"
                     /coded_by="NM_004917.1:1..765"
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       61 vhpqwvlsaa hcfqnsytig lglhsleadq epgsqmveas lsvrhpeyns pllandlmli
      121 kldesvsesd tirsisiasq cptagnsclv sgwgllangr mptvlqcvnv svvseevcsk
      181 lydplyhpsm fcaggghdqk dscngdsggp licngylqgl vsfgkapcgq vgvpgvytnl
      241 ckftewiekt vqas
//
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